1023-92-1576 **Dmitry A Kondrashov*** (dkon@biochem.wisc.edu), 433 Babcock Dr, Department of Biochemistry, University of Wisconsin - Madison, Madison, WI 53706, and **George N. Phillips** and **Joseph C. Watkins**. *Markov process modeling of biochemical reaction kinetics.*

Generally, all biomolecular processes are stochastic, noise-driven processes, for instance fluctuations of protein conformation, or diffusion of molecules in the cell. We present an analytical expression for kinetics of networks of Markov processes. We model the effects of conformational fluctuations in proteins on ligand binding and escape. For a small molecule binding to a site inside a protein structure, we build a model combining internal diffusion, stochastic gate between the heme cavity and the solvent, and rebinding and bond-breaking at the active site. The model addresses two mechanistic questions: how mobile, fluctuating structures control small ligand release in certain proteins, and why release rates differ in proteins possessing an identical binding site and a similar external gate. Other applications include computation of higher moments for the waiting time distribution in networks of Markovian reactions, and application to single-molecule and in vivo measurements. (Received September 26, 2006)